

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

# OM protein - protein search, using sw model

Run on: December 19, 2002, 14:53:07 ; Search time 38 Seconds  
(without alignments)  
3079.862 Million cell updates/sec

Title: US-08-813-323b-2

Perfect score: 3008

Sequence: 1 MESSKMDSPGALQTNPPK.....IKDDTIFIKYVDTSDLPDP 568

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_21:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriophage:\*  
17: sp\_archaeal:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1253.5	41.7	558	11	061480	061480 mus musculus
2	1253.5	41.7	558	11	P70191	P70191 mus musculus
3	1192.5	39.6	557	4	000463	000463 homo sapien
4	832	27.7	508	11	054896	054896 mus musculus
5	717	23.8	447	4	096N72	096N72 homo sapien
6	692	23.0	501	13	090W76	090W76 carassius a
7	560.5	18.6	470	4	014848	014848 homo sapien
8	560.5	18.6	470	4	09B024	09B024 homo sapien
9	553	18.4	522	4	09Y4K3	09Y4K3 homo sapien
10	536	17.8	530	11	P70196	P70196 mus musculus
11	524.5	17.4	462	5	09B1W7	09B1W7 caenorhabdi
12	522.5	17.4	462	5	09B1W7	09B1W7 caenorhabdi
13	522.5	17.4	462	5	063248	063248 drosophila
14	506	16.8	486	5	09Y1R0	09Y1R0 drosophila
15	503	16.7	412	5	090AC5	090AC5 drosophila
16	437.5	14.5	352	6	0951R1	0951R1 macaca fasc

17	286	9.5	296	12	080UJ9	080UJ9 infectious
18	286	9.5	452	5	0960H6	0960H6 drosophila
19	270	9.0	475	5	090AC4	090AC4 drosophila
20	270	9.0	475	5	09W319	09W319 drosophila
21	268	8.9	463	5	09YX09	09YX09 drosophila
22	263	8.7	395	5	09YXG5	09YXG5 drosophila
23	214.5	7.1	198	4	075615	075615 homo sapien
24	211	7.0	239	11	09CQ29	09CQ29 mus musculus
25	209.5	7.0	594	11	0922B6	0922B6 mus musculus
26	207.5	6.9	594	4	09H073	09H073 homo sapien
27	207	6.9	360	4	096CC2	096CC2 homo sapien
28	204.5	6.8	1063	11	090Y55	090Y55 mus musculus
29	203.5	6.8	1098	4	09UP07	09UP07 homo sapien
30	183.5	6.1	528	13	091885	091885 xenopus lae
31	182.5	6.1	335	5	09N886	09N886 caenorhabdi
32	173.5	5.8	313	10	09C6H3	09C6H3 arabidopsis
33	171	5.7	891	4	09Y2K3	09Y2K3 homo sapien
34	167	5.6	33	4	09UNL1	09UNL1 homo sapien
35	160	5.3	626	11	0922N9	0922N9 mus musculus
36	158	5.3	808	4	015083	015083 homo sapien
37	154	5.1	610	13	091431	091431 xenopus lae
38	153.5	5.1	1120	4	096EL5	096EL5 homo sapien
39	152.5	5.1	390	5	09VSW7	09VSW7 drosophila
40	152.5	5.1	609	13	092021	092021 xenopus lae
41	152.5	5.1	713	13	09YHD6	09YHD6 rana catesb
42	152	5.1	846	4	075130	075130 homo sapien
43	151.5	5.0	671	11	08R205	08R205 mus musculus
44	151	5.0	1938	13	091BD7	091BD7 seriola dum
45	150.5	5.0	1300	4	013999	013999 homo sapien

## ALIGNMENTS

RESULT 1  
ID 061480 PRELIMINARY; PRT; 558 AA.  
AC 061480;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE TRAF5.  
GN TRAF5.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC SPTREMBL\_21/C;  
RX MEDLINE=96278943; PubMed=8663299;  
RA Nakano H., Oshima H., Chung W., Williams-Abbott L., Ware C.F.,  
RT "TRAF5, an activator of NF-kappaB and putative signal transducer for  
the lymphotoxin-beta receptor.";  
RL J. Biol. Chem. 271:14661-14664(1996).  
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
DR MBL: D78141; BAAL1218.1; -  
DR MGD: MGI:107548; TRAF5.  
DR InterPro: IPR002083; TRAF.  
DR InterPro: IPR003007; TRAF.  
DR InterPro: IPR001841; Znf\_TRAF.  
DR InterPro: IPR001293; Znf\_TRAF.  
DR Pfam: PF000917; MATH; 1.  
DR Pfam: PF000927; Zf-C3HC4; 1.  
DR Pfam: PF02176; Zf-TRAF; 2.  
DR SMART: SM00061; MATH; 1.  
DR SMART: SM00184; RING; 1.  
DR PROSITE: PS00518; ZF\_RING\_1; 1.  
KW ZINC-FINGER.  
SQ SEQUENCE 558 AA: 64154 MW: D85E486746225042 CRC64;  
Query Match 41.7%; Score 1253.5; DB 11; Length 558;

Best Local Similarity 41.6%; Pred. No. 8.9e-71;  
Matches 241; Conservative 114; Mismatches 166; Indels 59; Gaps 10.

QY	22	HTDSAGP--VEVEEGD-----YKFKFVEDYKCKCHLYLCSPTQCGH	70
Db	3	HSEQAAVPCAFITQNSGNSISLDFEDPTEQVPEQLEERYKCAFISVTLHNQTCGH	62
QY	71	RFCECMAALLS--SSSPKTAQGEISVYKDYKFNCKCKRETLAQICRNESKCAEOLT	129
Db	63	RFCCOQIRSLRELSLVSPICPADKEVILPOEFYKFNCKCKRETLNHYVCN--APGCNARI	121
QY	130	LGHLLVHKNCNCHHEELPCVAPDCKEKVLRKDLDBHEKCAKCYEATCSCKSQVPIAL	189
Db	122	LGRQDHLQH--CSQAVPCPNESCSEEMLRKDVAKHEHLSAYCRFEKCKLYCKRDIVTNL	180
QY	190	OKHEDTDCPCVWCSPHKCSVOTLLRSELNAHLSECVNAPSTCSFKRRCGVQGTNOQIK	249
Db	181	QDHENSCSPAVPASCPRNC--VQTIIPRAVNHETLVCEAEQDCCPFKHGCTYKQKRGNTL	239
QY	250	AHEASSAVQHNLLKEMSNLSLEKRVSLLONESYKKNKSIOSLNQTOSFELEIRCKEML	309
Db	240	EHERRAALQDMLLVLEKNYOLEQRIISDLYOSLEQKESKIQQLAETVKEFEKLQFQFM	299
QY	310	RNN-----ESKILHLORVDSOAERKLELDKRIEPRQWMEADS	349
Db	300	GRNGTFILSNVQALSHDCKSMLEAQVRHLLQIYNQPSRL-----DLRS	344
QY	350	MKSSVESLQNFVTELESVDKSAGOVANRTQILLESQLSRHDOMLSVHDIRLADMLRFOVL	409
Db	345	LYDVAVDSVKQRIQTGLEASD-----ORLVLEEGESTKHDAHNIHKAOLNKMEERKOL	397
QY	410	ETASVNGVLIKIDYKRKRKEAVMGKTLISYSPFTGYGYCMARVLLNGDMKGT	469
Db	398	EGACTSGKLTKVYDIRYKRRKEAVEGHTVSFSSPFTTSCRGYLCARAILNGDSKGT	457
QY	470	HLSEFVIMRGEYDALLPWPFKQKVTYLMLDQSSRRHLGDAEKPDPNSSFFKPTGEMN	529
Db	458	HLSEFYVMREPEFSLLOMPFRQVYTTMLLDQSKKMHVETFEKADPNSSFFKRPDGMN	517
QY	530	IASGCPVFAQTVLEN--GVYIKQDTIFIKYIVQTSPLD	567
Db	518	IASGCPRVYSHSTLENSKNYTIKQDTLFLKAVAVDITLDED	557
RESULT 2			
P70191		PRELIMINARY; PRT; 558 AA.	
AC	P70191		
DT	01-FEB-1997 (TREMblrel. 02, Created)		
DT	01-FEB-1997 (TREMblrel. 02, Last sequence update)		
DT	01-JUN-2002 (TREMblrel. 21, Last annotation update)		
DE	TRAF5 (Similar to TNF receptor-associated factor 5).		
GN	TRAF5.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
CC	Mammalia; Euthera; Rodentia; Sciurognath; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RN	SEQUENCE FROM N.A.		
RX	MEDLINE=96382484; PubMed=9790348;		
RA	Isidra T., Tojo T., Aoki T., Kobayashi N., Ohishi T., Watanabe T.,		
RA	Yamamoto T., Inoue J.;		
RT	"TRAF5, a novel tumor necrosis factor receptor-associated factor		
RT	family protein, mediates CD40 signaling."		
RL	Proc. Natl. Acad. Sci. U.S.A. 93:9437-9442(1996).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE-COLON;		
RA	Strausberg R.;		
CC	Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.		
EMBL	D83528; BA011942.1; -.		
DR	EMBL; BC012702; AA012702.1; -.		

DR MGD: MG1:107548; Traf5.  
DR InterPro: IPR002083; MATH.  
DR InterPro: IPR003007; TRAF.  
DR InterPro: IPR001841; ZnF\_RING.  
DR InterPro: IPR001293; ZnF\_TRAF.  
DR Pfam: PF00917; MATH; 1.  
DR Pfam: PF00097; ZF-C3HC4; 1.  
DR Pfam: PF02176; ZF-TRAF; 2.  
DR SMART: SM00061; MATH; 1.  
DR SMART: SM00184; RING; 1.  
DR PROSITE: PS00518; ZF\_RING\_1; 1.  
DR Receptor; Zinc-finger.  
KW SEQUENCE 558 AA; 64145 MW; 48b64fB83bd587b5 CRC64;

Query Match	41.7%;	Score 1253.5;	DB 11;	Length 558;
Best Local Similarity	42.9%;	Pred. No. 8.9e-71;		
Matches 243;	Conservative 116;	Mismatches 176;	Indels 31;	Gaps 11;

QY	22	HTDRBACGR-VFVPEBGG-----YKRFKVTEDXKCKCKHLYLCSPPQECGH	70
Db	3	HSEEDAAVPCAFIRKQNSNSISLDFEPDTQVQFQLEERKCAFCHSVLHNPQTCGH	62
OY	71	RFCECMAMALAS-SSSPKCTACQESIYVDKVFKNQCKRETLAQIYCRNESCACOLT	125
Db	63	RFQOOCISLSELNSVPLCPDPKDEYIKQFVFKQNCREVLNLAHYCKN-APCCNARI	121
QY	130	LGHLLVHLKNDQHEEELPCVBPDKCEKYLKRDLDHYEACKRYEATCSCKSOVPAL	189
Db	122	LGRFDQHLQH-CSFQAVPCPNESCREALRKDQVEKHLNAYCFRFEKCLYCKRDIYVTL	186
QY	190	QKHEDTDCPCVYVSCPHKCSQVTLIRSLSLHSECVNAPSTCFKRYGCVFOSTNOIK	249
Db	181	QDHENSCPCAPVSPQBNBC-VQIIPRAVKNHLLVCPREADQCFKHGCTVKKRGNLL	238
OY	250	AHEASSAOVHNLKEMNSLEKRYSLQJNSESVEKNKSIQSLHNOICSFEEIEBREM	308
Db	240	EHERRALDDHMLVLEKQYQLEQKRLSDLYQSLQDEKESLQQLATVYKFEELKQFQMF	299
QY	310	RNNESKLIHLQVIDISQAELKELEKDEIRPRQ--NME---EADSMKSSYESIQNRVTE	365
Db	300	GRNGFTLSNQ-ALTSHTDKSAMLEAQVROLQIYNQOPSRDLRLSLVDAVDYSKORITQ	358
QY	364	LESVDKSGQVYARNGLLESQLSRHDQMLSHVDRILAMDRLPOVLEFASVNGVLIKIR	422
Db	359	LEASD-----QRLVLELGETSKSHDAHINHHKQALKNKERRFQOLBQACSGKLIMKV	411
OY	424	DYKRRQEAVMGKTLSTLYSOEFTYGFEGYKKACARVYLLGDGMSGKTHLSLFTVMRREYD	483
Db	412	DYRKVKRRVAEGSHVYSVSOFPYTSRCYRLCARAYLLINDGDSGKTHLSLFTVMRREYD	471
QY	484	ALLPWFQKVATLMLMDGSSRRHLGDAFKDPDPNSSSFKKFTGEMNTIASGCPVFAQTVL	543
Db	472	SLQMPFRQVATLMLMDGSKNHIVETFKADPDPNSSFRRPDGEMNTIASGCPFRVSHSTL	531
QY	544	EN--GTIYKDDTIFIKVYLVDSLDP	567
Db	532	ENSKNTYIKDDTFLPKAVADLTLED	557

RX MEDLINE=98172745; PubMed=9511754;  
 RA Mizushima S., Fujita M., Ishida T., Azuma S., Kato K., Hirai M.,  
 RA Otsuka M., Yamamoto T., Inoue J.;  
 RT "Cloning and characterization of a cDNA encoding the human homolog of  
 RT tumor necrosis factor receptor-associated factor 5 (TRAF5).";  
 RL Gene 207:135-140(1998).  
 RN [2]  
 RN SEQUENCE OF 20-557 FROM N.A.  
 RX MEDLINE=97321041; PubMed=9177772;  
 RA Nakano H., Shindo M., Yamada K., Yoshida M.C., Santee S.M., Ware C.F.,  
 RA Jenkins N.A., Gilbert D.J., Yagita H., Copeland N.G., Okumura K.;  
 RT "Human TNF receptor-associated factor 5 (TRAF5): cDNA cloning,  
 RT expression and assignment of the TRAF5 gene to chromosome 1q32.";  
 RL Genomics 42:26-32(1997).  
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
 DR EMBL: AB000509; BAA25262.1; -;  
 DR EMBL: U69108; AAC51329.1; -;  
 DR InterPro: IPR002083; MATH.  
 DR InterPro: IPR003007; TRAF.  
 DR InterPro: IPR001841; ZnF\_RING.  
 DR InterPro: IPR001293; ZnF\_TRAF.  
 DR Pfam: PF00917; MATH; 1.  
 DR Pfam: PF00097; zf-C3HC4; 1.  
 DR Pfam: PF02176; zf-TRAF; 2.  
 DR SMART: SM00061; MATH; 1.  
 DR SMART: SM00184; RING; 1.  
 DR PROSITE: PS00518; ZF\_RING\_1; 1.  
 DR Zinc-finger.  
 SQ SEQUENCE 557 AA; 64405 MW; 86EB3724CE11176 CRC64;  
 Query Match 39.6%; Score 1192.5; DB 4; Length 557;  
 Best Local Similarity 42.0%; Pred. No. 5.9e-67;  
 Matches 232; Conservative 121; Mismatches 178; Indels 21; Gaps 9;  
 QY 25 RSAGTPVFEVPEQGYKEKFKVTEEDKYKCEKCHLVCSPKQTEGCHRCESCMALLS-S 83  
 DB 17 QNSGTSISIDPFSIEGYFVERLERKYPACPHSHLPHNGCGHRCQCHCITLSRLN 76  
 QY 84 SSPKCTACQESTIVKDKVFKNCCCKREIILALQICRNESBGCALQTLGHLVHLKNDCHF 143  
 DB 77 TVPICVDREKIVKIQEVEFNDCKREVLVLYYCSN-APGCAKAYILGRYDHDLO-QCLF 134  
 QY 144 EELPCVRPRCKEVLKRDLDHVEKACKYREATCSHCKSQVPMILQKHEDPCCVVVS 203  
 DB 135 QPQCSNEKCRVPLKDKLHLSASQCRKCKLYCKKDVVYVILQNHENLCEPIYVF 194  
 QY 204 CPHKCSVQTLRLSELSEHLSECUNAPSTCSFKRYGCVFQGTNOQIKAHASSAVQHVNL 263  
 DB 195 CPANCA-KIILKTEVDEHLAVCPREADQCPFKHYGCAVTDKRRNLQDHEHSHALREHMLV 253  
 QY 264 KEKSNLEKKVSLQNESVEKKNKSLOSILNOICSPFIEIERQKEMIRNNEKILHLQRYI 323  
 DB 254 LKKNVLEEDQIDSLHKSLSQKESKIQDLAETTKLEKEKQKQAPLQKNGSFLPNIO-VF 312  
 QY 324 DSOAKELKELKEIRPF-----RQNMEDADSKSSVESLQNRVTELESVDKSGQVARN 377  
 DB 313 ASHITDSANLEAOVHQLLOMVOQOKKEDRLPLMEAVDQVOKITLLEND-----QR 365  
 QY 378 TGLLESQLSHNDMLSVHDIRLADMDLRFQVLETASYNGLVINKIRIDYRRKROEAVMGKT 437  
 DB 366 LAVLEETNKHDTNHNHKNQKLSKNEERFKLEGTCTYCNKLIWKVYDKMKRKAADGHT 425  
 QY 438 LSLYSGPFTYGYGYKMCARVYINGQMKGTHLSFFVIMGEVYALLPMPKQVTLML 497  
 DB 426 VSTFSOSFYRSGYRCAYALYNGDSGSGSHLSLYFVVMKEEFSLLQMPFRQVYTLM 485  
 QY 498 LMDGSRRLHGDARFDPNNSFFKPTGEMINIASGCPVFAQTVLEN--GTYIKDITLF 555  
 DB 486 LLQD-SKKKIMETFKRDPNNSFFKRPDGEMLIASGCPRVAVSHVLENKKNAYIKDITLF 544  
 QY 556 IKVIYDTSLLPD 567  
 DB 545 LKVAVDLTDLDD 556

RESULT 4  
 ID 054896 PRELIMINARY; PRT; 508 AA.  
 AC 054896;  
 DT 01-JUN-1998 (TREMBLrel. 06, Created)  
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Tumor necrosis factor receptor associated factor 2A.  
 GN TRAF2A.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 ON NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=KIDNEY;  
 RX MEDLINE=98129826; PubMed=9461607;  
 RA Brink R., Lodish H.F.;  
 RT "Tumor necrosis factor receptor (TNFR)-associated factor 2A (TRAF2A),  
 RT a TRAF2 splice variant with an extended RING finger domain that  
 RT inhibits TNFR2-mediated NF-kappaB activation.";  
 RL J. Biol. Chem. 273:4129-4134(1998).  
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
 DR EMBL: AF027570; AAC53545.1; -;  
 DR HSSP: P12351; 1HMT.  
 DR InterPro: IPR002083; MATH.  
 DR InterPro: IPR003007; TRAF.  
 DR InterPro: IPR001841; ZnF\_RING.  
 DR InterPro: IPR001293; ZnF\_TRAF.  
 DR Pfam: PF00917; MATH; 1.  
 DR Pfam: PF00097; zf-C3HC4; 1.  
 DR Pfam: PF02176; zf-TRAF; 2.  
 DR SMART: SM00061; MATH; 1.  
 DR SMART: SM00184; RING; 1.  
 DR PROSITE: PS00518; ZF\_RING\_1; 1.  
 DR Receptor; zinc-finger.  
 SQ SEQUENCE 508 AA; 56757 MW; 74B8B26BFC9B1C4 CRC64;  
 Query Match 27.7%; Score 832; DB 11; Length 508;  
 Best Local Similarity 33.7%; Pred. No. 2e-44;  
 Matches 199; Conservative 90; Mismatches 190; Indels 112; Gaps 19;  
 QY 3 SSKMDSPGALQTNPLKLTDRSAGTPVFEQGYKEKFKVKT-VEDKYKCEKCHLVLC 61  
 DB 2 AAAYTSPGSELLOP-----GSKTLGRLAKYLCASCKNILR 42  
 QY 62 SPKQTEGCHRCESCM-----AALLSSSPK-CTAC-----QEST---VKDKVFDNC 105  
 DB 43 RPFQACGHRYSFCLTSLNCASILLSSGSPONCAACVDEGLYEGISILSSSAFPDMA 102  
 QY 106 CKREILALQICRNESRSCALQTLGHLVHLKDKCHEELPCVRPCKEVLKRDJRD 165  
 DB 103 ARREVESIPAVCPND--GCTWKGTLEKYESCHBGLCPFLTEC--PACKGLVRLSEKHN 158  
 QY 166 VEKAKYREATCSHCKSGVPMIALQKHEDTDCPVVNSCPHKCSVQTLRLSELSEHLSEC 225  
 DB 159 TQDECPKRLSLSCQHRARCSHVDELVNEYV-CPKRPFLTC-DGCGKKKIPRETPODHYRAC 216  
 QY 226 VNAPSTCSFKRYGCVFQGTNOQIKAHASSAVQHVNLKEMSNLEKKVS----- 275  
 DB 217 SKCRVLCFHHVYVGSSEVETENLDHELRRLREHLAL--LSFLEQASGTLNVOGRE 274  
 QY 276 ILQNSVVRKNKSLOSILNOICSPFIEIERQKEMIRNNEKILHLQRYVDSQAEKLELDK 335  
 DB 275 ILQKQOILEQK-TATFENIVCYLREVER-----VAAYTAEKCSQHRLDQ 318  
 QY 336 EIRPFRQNMEDADSKSSVESLQNRVTELESVDKSGQVARNGLLESQLSRHNDMLSVH 395  
 DB 319 D-----KTEALSNKVQOLE-----RSIGL-----K 338  
 QY 396 DIRLADMDLRFQVLETASYNGLVINKIRIDYRRKROEAVMGKTLISLYSGPFTGYGYKMC 455

QY 303 ERCKEKLNRNNKSLIHLQVRIDSAQELKELDEIRFRQNMEEADSMKSSVESIQNVVT 362  
 Db 250 -----PREFFQODK-----TEALSSVQ 268  
 QY 363 ELESYDKSAGVARNITGLLESQLSRHDOMLVHDIRLADMDFVOYLEATSYNGVLIRKI 422  
 Db 269 QLE-----RSIGL-----KDLAMADEQGLEVEASTVDGVFIKI 304  
 QY 423 RYKRRKOEAVMGKTLISYQPEFYGYGKMKARYLNGDMGKGTHTLSLFVYIMREY 482  
 Db 305 SFPARKOEAVAGRPALFSPAFYTSRIGYKMLRLIYLDGDTGRTHTLSLFVYMKAPN 364  
 QY 483 DALLWPEKKKVTIYMLMDGSSRRHLDADKPPDNSSFRKPTGEMINTASGCVFVAQTV 542  
 Db 365 DALLWPEKKKVTIYMLMDQ--NNREHVIDARPDVTSSSPQRPVNMNIASGCLPECPYK 423  
 QY 543 LE-NGTYIKDDTIFIKIYVTSDL 565  
 Db 424 MEAKNSYVRDDAIFIKAIYDLTGL 447  
 RESULT 6  
 O90WT6 PRELIMINARY; PRT; 501 AA.  
 AC O90WT6;  
 DT 01-DEC-2001 (Tremblrel, 19, Created)  
 DT 01-DEC-2001 (Tremblrel, 19, Last sequence update)  
 DT 01-MAR-2002 (Tremblrel, 20, Last annotation update)  
 DE Tumor necrosis factor receptor associate factor-2.  
 GN TRAF2.  
 OS Carassius auratus (Goldfish).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Carassius.  
 OX NCBI\_Taxid=9577;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Wang T., Secombes C.J.;  
 RT "Cloning and expression of crutian carp tumor necrosis factor receptor  
 RT associate factor-2 (TRAF2).";  
 RL Submitted (OCT-2000) to the EMBL/Genbank/DBJ databases.  
 CC -1- SIMILARITY: CONTAINS 1 KIN- TYPE ZINC FINGER.  
 CC EMBL; AJ297860; CACB2653.1; --  
 DR InterPro: IPR002083; MATH.  
 DR InterPro: IPR003007; TRAF.  
 DR InterPro: IPR001841; ZnfRING.  
 DR InterPro: IPR001293; Znf-TRAF.  
 DR Pfam: PF000917; MATH; 1.  
 DR Pfam: PF00097; Zf-C3HC4; 1.  
 DR Pfam: PF02176; Zf-TRAF; 2.  
 KW Receptor; zinc-finger.  
 KW SEQUENCE 501 AA; 56503 MW; DEDED0F8D9DC287 CRC64;  
 Query Match 23.0%; Score 692; DB 13; Length 501;  
 Best Local Similarity 30.7%; Pred. No. 1.2e-35;  
 Matches 159; Conservative 84; Mismatches 169; Indels 106; Gaps 14;  
 QY 40 KEKFKVTEDEKYKCECHLVLCSPKOTEGCHGFCSMAALLSSSPKCAQO-ESIVMD 98  
 Db 32 REVLSVSMERKYQCCQCKEILKRPQACGHRFCVFCRQUTLSSGPIPCACACADEIFEE 91  
 QY 99 KV-----FKDNCCKREITLALQYICRNESGCCAEOLTLGHLIVHLKNDCHFEELPCVR 150  
 Db 92 AMSMNLITVAFPDNNARRRIDSLPAKPCPD--GCSWSGTLKDYEGGHEGRCDPERVYC-- 147  
 QY 151 PDCKEYKVLKRDLDNHEKACKYREATCSHCKSYQPMIALKHEPTDPCPVVYSCPHKGSV 210  
 Db 148 EAQGVYVILSEKDRHNERCEAKTLNCKYCAVYTNFNEIKAHDEIT-CQKPRMOC-KDCGK 205  
 QY 211 QTLRLSELSAHLSECVNAPSTCSFKRYGCVFQGTNOQIKAHKSSAVOHVNL----- 263  
 Db 206 KKIPRKPFEHNRKCAKSKACSFCEIGCAVYDNGKQOEEDQTSVNEHRIYMLSVTSV 265

QY 264 -----KENSNSLEKVVSLQ-----NESVEK-----NKSTQSLHNOICS 297  
 DB 266 RLRAAGAGNOE--DSGLGRPEDAPAPGPNAAHAGGGPGVQOKTALENTVCV 323  
 QY 298 FEIEIEROKEMLRNNESIILHQRVIDSQAEKLEKDEKEIRPFQONWEADSMKSSVESL 357  
 DB 324 LNREVERSAITL-----EALSROHRLDQ-----KIENTL 352  
 QY 358 QNRVTELESVDKSAGQVARTGLLESQLSRHDQMLSVHDIRLADMRLFOVLETA5NGV 417  
 DB 353 SNKVRQLE-----RTLTMRDLQLAESQSLRELOFCTYDGV 388  
 QY 418 LMKIRDKRRKQEAVMKKTSLTSQPFYTGFGYKMKARVYLYNGDGKGTHTLSFEVI 477  
 DB 389 FIMKTADESRRQDAVGGRAAPMSPAFYSKYGKMLRLYLNGDGTGRTGSLFEVV 448  
 QY 478 MRGEVDALLPMPFKOKVTLMMDGSSRRHLGDAFKPD 515  
 DB 449 MRGYDALLKMPFSOKVTLMMLDQ--NNRHILDAFRPD 485

## RESULT 7

Q14848 PRELIMINARY: PRT: 470 AA.

AC Q14848: 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Cystein rich domain associated to RING and TRAF protein.  
 OS MLN 62, CART1.  
 OC Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-BREAST DERIVED METASTATIC LYMPH NODE;  
 RX MEDLINE=96039245; PubMed=7490069;  
 RA Tomasetto C., Regnier C.H., Moog-Lutz C., Mattel M.G., Chenard M.P.,  
 R Lidereau R., Basset P., Rio M.C.;  
 RT "Identification of four novel human genes amplified and overexpressed  
 in breast carcinoma and located to the q11-q21.3 region of chromosome  
 17";  
 RL Genomics 28:367-376(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-BREAST DERIVED METASTATIC LYMPH NODE;  
 RX MEDLINE=96029665; PubMed=7592751;  
 RA Regnier C.H., Tomasetto C., Moog-Lutz C., Chenard M.P., Wendling C.,  
 Basset P., Rio M.C.;  
 RT "Presence of a new conserved domain in CART1, a novel member of the  
 tumor necrosis factor receptor-associated protein family, which is  
 expressed in breast carcinoma.";  
 RL J. Biol. Chem. 270:25715-25721(1995).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-BREAST DERIVED METASTATIC LYMPH NODE;  
 RX MEDLINE=98173888; PubMed=9507120;  
 RA Masson R., Regnier C.H., Chenard M.P., Wendling C., Mattel M.G.,  
 Tomasetto C., Rio M.C.;  
 RT "Tumor necrosis factor receptor associated factor4 (TRAF4) expression  
 pattern during mouse development.";  
 RL Mech. Dev. 71:187-191(1998).  
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
 DR EMBL: X80200; CAA56491.1;  
 DR InterPro: IPR002083; MATH.  
 DR InterPro: IPR003007; TRAF.  
 DR InterPro: IPR001841; znf\_fing.  
 DR InterPro: IPR001293; znf-TRAF.  
 DR Pfam: PR000917; MATH; 1.  
 DR Pfam: PR00097; zf-C3HC4; 1.  
 DR Pfam: PR02176; zf-TRAF; 3.

DR SMART; SM00061; MATH; 1.  
 DR SMART; SM00184; RING; 1.  
 DR PROSITE; PS00518; zf\_RING\_1; 1.  
 KW Zinc-finger.  
 SQ SEQUENCE 470 AA; 53443 MW; 5D457ED5A78770E2 CRC64;

Query Match 18.6%; Score 560.5; DB 4; Length 470;  
 Best local Similarity 24.9%; Pred. No. 1,9e-27;  
 Matches 147; Conservative 75; Mismatches 173; Indels 195; Gaps 13;

QY 38 GYKEKPYVEDKYKCEKHLVCSPRQ--TEGCRPRCESCMALLSSSPKTCACQESIV 96  
 DB 3 GFDFKLEKPKRRLLCPGLCGKPMREPOVSTCGHRCDCLOFISEGVKCEPDLPID 62  
 QY 97 KDVFPKDNCKREITLQIYCRNESRGAQOLTLGHLLVHLKDKHFEELCPVRPD-CKE 155  
 DB 63 YAKIYDPELEVOYLPIPCIHSEBCRRSGRLRLQHL-NTGSFNVIYC--PKRCM 119  
 QY 156 KVLKDLRDHVERACKCREATCSHCKSQVPMIALQKHE----- 193  
 DB 120 KLSRDLPAHLQDCCPRRLKCEFCGDDFGSEAYESHGWCPOESYCEKKGARMRG 179  
 QY 194 -----DT-----DPCVYVSCPHKCSVOTLSELSAHL 222  
 DB 180 LAQHATSECPKRPCTCYCTKEEFVDTIOHQYOCPLPACPCNQCQGVTAHEDLPGLH 239  
 QY 223 SE-CVNAPSICSPFKRGCVPGTNOITKAHEASSAVQHVNLKENSLSLEKVVLLONES 281  
 DB 240 KDSQNTLVLCIPFDSCKIRCKLMARVIESVPHLMM----- 281  
 QY 282 VEKNKSIOSLHNOICSPFEIEIEROKEMLRNNESIILHQRVIDSQAEKLEKDEKEIRPF 341  
 DB 282 -----CA-----LVSRQRELDELREL----- 299  
 QY 342 QNWEADSMKSSVSLQNRVTELESVDKSAGQVARTGLLESQLSRHDQMLSVHDIRLAD 401  
 DB 300 -----EELSV----- 304  
 QY 402 MDLRFVLETA5NGVLMKIRDKRRKQEAVMKKTSLTSQPFYTGFGYKMKARVYLYN 461  
 DB 305 -----GSGCVLIMKIGSGRLQEKAKAPNLECSPAFYTHKYGKLOVSAFLN 353

QY 462 GDGKGTHTLSLFEVIMGEYDALLPMPFKOKVTLMMDG-----SSRHLGDAFKDPN 517  
 DB 354 GNGSGEGHTLSLTRYLVGAFDNLEMPFARVYFSLDSDPOLAKPOHYTEFFHDPN 413  
 QY 518 SSSFRKP-----TGMNIIASGCPVFAQVYLENGTYIKDITFIKVIYD 561  
 DB 414 WKNFQKPGTWRGSLDESLGFGYFKFTSHODIRKRNRYRDDAVITRAVE 463

## RESULT 8

Q9BUZ4 PRELIMINARY: PRT: 470 AA.

AC Q9BUZ4: 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE TNF receptor-associated factor 4.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-EYE;  
 RA Strausberg R.;  
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
 DR EMBL: BC001769; AA01769.1;  
 DR InterPro: IPR002083; MATH.  
 DR InterPro: IPR003007; TRAF.  
 DR InterPro: IPR001841; znf\_fing.

DR InterPro: IPR001293; Znf\_TRAF.  
 DR Pfam: PF00917; MATH; 1.  
 DR Pfam: PF00917; zf-C3HC4; 1.  
 DR Pfam: PF02176; zf-TRAF; 3.  
 DR SMART: SM00061; MATH; 1.  
 DR SMART: SM00184; RING; 1.  
 DR PROSITE: PS00518; ZF\_RING\_1; 1.  
 DR Receptor: Zinc-finger.  
 KW Receptor; Zinc-finger.  
 SO SEQUENCE 470 AA; 53542 MW; A3F57E0E1081AB8 CRC64;

Query Match 18.6%; Score 560.5; DB 4; Length 470;  
 Best Local Similarity 24.9%; Pred. No. 1.9e-27;  
 Matches 147; Conservative 75; Mismatches 173; Indels 195; Gaps 13;

QY 38 GYKFKVYKVEDYKCEKCHLVLCSPKQTEGCHRCESCMALLSSSPKCTACQESIV 96  
 DB 3 GFYKFLKPKRRLCLPCLGKPRKREPVQVSTGCHRCDCLOEFLSEGVKCPEDOLP 62  
 QY 97 KDKVFNCKCKREILALQIYCRNRCGAEOULTLGHVNLKNDCHFEELPCVPRPD-CKE 155  
 DB 63 YAKYDPDELEVQVLGLPIRCIHSEGCRCWSPRLRHLOGLH-NTCSFNVIIC--FNRCPM 119  
 QY 156 KYIKRLRQHVKEKCKYKREATCSHCKSQVPMALQKHE----- 193  
 DB 120 KLSRRLPAHLQHDCEKRLKCEFCGDESGEAYSHHEGMCPOESVYCCNKCGAMMRRL 179  
 QY 194 -----DPCVYVSCPHKCSVOYTLRSELSAHL 222  
 DB 180 LAQHATSECPKRPCTCTCTKEFVDTIQSHQYCPRLPVAQPCQGVGTVARDELPHGL 239  
 QY 223 SE-CVNAPTSCFKRKYGVQGTNOQIKAHSSAVOHVNLKENSLEKVSILLONES 281  
 DB 240 KQSCNTALVCPFKSGCKHRCPLAMARHVESVYKPHLAM----- 281  
 QY 282 VEKNKSIOSLHNOICFSEIEIRKEMLNNSKILHLQVIVDSQAEKLEKDEIRPER 341  
 DB 282 -----CA-----LYSRROELQELREL----- 299  
 QY 342 QWNEADSKSVESLQNVTELESVDKSAGAVARNTGLLESQLSRHDOMLSVHDIRLAD 401  
 DB 300 -----ELLSV----- 304  
 QY 402 MDLRQVLETASYNGVLWIKIRKROEAMGKTLISYQPTFTGYKMKCARVYLN 461  
 DB 305 -----GSDGVLLWIKIGSYGRLOEAKAKPNLECFSPAFYTHHYGKYLQVSAPLN 353  
 QY 462 GDGKMGKTHLSLFVIMRGEYDALPMPFKOKVITLMDOG-----SSRRHIGDAFKPPDN 517  
 DB 354 GNGSGEGHLSYIVRLGARDNLEWPFARVYTSLLDQSDPLAKFOHVTETHPDPN 413  
 QY 518 SSSFKP-----TGENNIASGCPVFAQVLENGTYIKDDTIFIKVIVD 561  
 DB 414 WNFQKPGTWNGSLDESSLGFYGFISHODIRKKNYVRDVAVIRAAVE 463

## RESULT 9

QY4K3 PRELIMINARY; PRT; 522 AA.  
 AC QY4K3;  
 DT 01-NOV-1999 (TREMBLrel. 12, Created)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Putative Interleukin 1 signal transducer.  
 GN TRAF6.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N. A.  
 RA MEDLINE=96434892; PubMed=8837778;  
 RA Cao Z., Xiong J., Takeuchi M., Kurama T., Goeddel D.V.;  
 RT "TRAF6 is a signal transducer for interleukin-1."

RL Nature 383:443-446(1996).  
 CC - SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
 DR EMBL: U78798; AAB8751.1; -.  
 DR HSSP: P15919; IRMD.  
 DR InterPro: IPR002083; MATH.  
 DR InterPro: IPR00504; RNA\_rec\_mot.  
 DR InterPro: IPR003007; TRAF.  
 DR InterPro: IPR001841; Znf\_Ting.  
 DR InterPro: IPR001293; Znf\_TRAF.  
 DR Pfam: PF00917; MATH; 1.  
 DR Pfam: PF00917; zf-C3HC4; 1.  
 DR Pfam: PF02176; zf-TRAF; 2.  
 DR SMART: SM00061; MATH; 1.  
 DR SMART: SM00184; RING; 1.  
 DR PROSITE: PS00030; RRM\_RNP\_1; UNKNOWN\_1.  
 DR PROSITE: PS00518; ZF\_RING\_1; 1.  
 KW Zinc-finger.  
 SO SEQUENCE 522 AA; 59573 MW; 5AB9C255CFF749 CRC64;

Query Match 18.4%; Score 553; DB 4; Length 522;  
 Best Local Similarity 26.7%; Pred. No. 6.4e-27;  
 Matches 144; Conservative 101; Mismatches 199; Indels 96; Gaps 16;

QY 32 FVPEGGYKKEKFKVTEEDYKCEKCHLVLCSPKQTEGCHRCESCMALLSSSPKCTAC 91  
 DB 49 FMEIIGYDVEFDEPRLSKYTCPCICMLARNAVOTPCGHFCACITIKSIDAGHKCPVD 108  
 QY 92 QESYKDKVFNCKCKREILALQIYCRNRCGAEOULTLGHVNLKNDCHFEELPCVPR 151  
 DB 109 NEILLEQVLPFNDAKREILSLWKCPE--GCILHKKELHLNLDH-QAHCEFALMPC--P 163  
 QY 152 DCKEVLKRLDRDQHVKEKCKYKREATCSHCKSQVPMALQKHEPDPCVYVSCPHKCSVQ 211  
 DB 164 QCGPRFQKFNHINHLKDCRRQVSCNCAASAFDEKELH-DONCPVANICEY-CNT- 220  
 QY 212 TLRLSELSAHL-ECVNAPTSCFKRKYGVQGTNOQIKAHSSAVOHVNLKENSLE 270  
 DB 221 ILIREQMPNHVDLDCPPAPIPCTFSTGCEHKQMRHLARHLQENQSHMRMLAQVHSL 280  
 QY 271 EKKVSLQNSVEKNKSIOSLHNOICFSEIEIRKEMLNNSKILHLQVIVDSQAEK 330  
 DB 281 -----SVLPDSGYIS--EVNRFQETIQLQEGRLVRODHOIRELTAKMETQSMYV 327  
 QY 331 KELDEIRPROMNEADSKSVESLQNVTELESVDKSAGAVARNTGLLESQLSRHQ 390  
 DB 328 SELKRTIR-----TLEDKVALIEA----- 346  
 QY 391 MLSVHDIRLADMRLFOVLETASYNGVLWIKIRDY---KRRQEAVMGKTLISYQSPY 446  
 DB 347 -----QQCNGLIYIKIGNFGMHLKQDEE---KPVYIHSPPGY 381  
 QY 447 TGYFGYKMKARVYLN-GDGKMGKTHLSLFVIMRGEYDALPMPFKOKVITLMDOGSS- 504  
 DB 382 TGRKGYLQKRLHLDLPQARCANYSLEFVNIMOGEDSHLPMPFGTIRLTLLDSEAP 441  
 QY 505 -RRHLGDAFKPDNSSSFKKTGEMNIAS-GCPVFAQVLENGTYIKDDTIFIKVIVT 562  
 DB 442 VRQNHHEIMAKRELLAFQRTIPRNPKRGYVTFHNLALQRTIKDDTILLVRCVST 501

## RESULT 10

P70196 PRELIMINARY; PRT; 530 AA.  
 AC P70196;  
 DT 01-FEB-1997 (TREMBLrel. 02, Created)  
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE TRAF6.  
 GN TRAF6.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;

```

RN [1]
RP SEQUENCE FROM N.A.
RA Inoue J.;
RT "TRAF6, a novel CD40 associated factor.";
RL J. Biol. Chem. 0:0-0(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE-97067112; PubMed-8910514;
RA Ishida T., Mizushima S., Azuma S., Kobayashi N., Tojo T., Suzuki K.,
RA Aizawa S., Matsumoto T., Mostoslav G., Kleff E., Yamamoto T., Inoue J.;
RT "Identification of TRAF6, a novel tumor necrosis factor receptor
RT associated factor protein that mediates signaling from an amino
RT terminal domain of the CD40 cytoplasmic region.";
RL J. Biol. Chem. 271:28745-28748(1996).
CC -1 SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: D84655; BAA12705.1;
DR HSSP: P15919; 1RMD
DR MGD: MGI:108072; Tiaf6.
DR InterPro: IPR002083; MATH.
DR InterPro: IPR000504; RNA_rec_mot.
DR InterPro: IPR003007; TRAF.
DR InterPro: IPR001841; znf_ring.
DR InterPro: IPR001293; znf_TRAF.
DR Pfam: PF00917; MATH; 1.
DR Pfam: PF00097; zf-C3HC4; 1.
DR Pfam: PF02176; zf-TRAF; 2.
DR SMART: SM00061; MATH; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS00030; RRM_RNP_1; UNKNOWN_1.
DR PROSITE: PS00518; zf_RING_1; 1.
KW Zinc-finger.
SQ
SEQUENCE 530 AA: 60082 MW: 9920820B4CEDB85B CRC64;

Query Match 17.8%; Score 536; DB 11; Length 530;
Best Local Similarity 25.7%; Pred. No. 7, 5e-26;
Matches 141; Conservative 97; Mismatches 206; Indels 104; Gaps 17;

OY 32 FPEBGGYKREKVEKVEDEKYEKCHLVLCSPKQTEGCHRFCECMAALLSSSPKCTAC 91
DB 49 FMEELQGYDVEDEPRLSEKYECPICLMLREAVQPCGHRFCACIIKSIDAGHKCPVD 108
OY 92 OESYKDYKFNCKCKRELLAOIYCRNBSRGAQOLILGLHLVILKNDKCFEELPCVRP 151
DB 109 NEILLENDLPFNFAKREILSLITVACPN--KGLQAKMELRLHEDH--OVNCEPALVNC--P 163
OY 152 DCKEVLRLKLDHVEKAKYREATCSHCKSOVMIALQKH--EDTDCPCVVVSCPHKCSV 210
DB 164 OCQRFQKQCVVTHIIECDPRQVSCVNC--AVSMAYEEKEIHQDSGLANIIQCY--CGT 220
OY 211 QTLRLSELNHLN--ECVAPSTCSFKRGCVFOGTNOQIKAHESASAVOHVNLKEMSNS 269
DB 221 -ILIEQPNHNDLDCPPAPIPCTFFSVFGCHQKQKQNRHLNHLQENLOLHMRLL----- 273
OY 270 LEKKVSLQNSVEKNKSIQSLHNOICFELIEEROKEMLRNNSKILHLQVIDSOAK 329
DB 274 -----AQAVHNNTAL-----RPDASp- 292
OY 330 LKELDKELRPRRQNMEEADSKSSVESIQNRV-----TELSVDKSAQOVARNT 378
DB 293 -----SRGCRPEDPNVEE-----TIKQLESRLVRODHOIRELTAKMETQSVGELKRTI 342
OY 379 GLLSOLSRHDOMLSVHDIRLADMRLROVLETASYNQVLTKRDKRRKQZEVNMGKTL 438
DB 343 RTLEKVAE-----MEAOQCMGKITWKLKGFQGMHLKSOEEBRPV 381
OY 439 SLYSQPEYTYGYGKMCARVYLN--GDGNGKSTHLSLFVIRGSEYDALLPWFQKVTLM 497
DB 382 VHSFGFTGPRGYKLCRLHLQPLTAQRCAANYISLVTHMGEGYDHLRPREPGTIRLT 441
OY 498 LMDQGS--RRHLGDAFRPDPNSSFFKPTGEMNIAS--GCFVFAQTVLLENGTVIKDDTI 554
DB 442 ILDSSEALIRQNHHEVMDAKPELLAFQRPITPRNPKGFGVYTFMHLBALRQGTIKDDTL 501

```

```

OY 555 FIKVIYDT 562
DB 502 LVRCVST 509

RESULT 11
ID 061382 PRELIMINARY; PRT; 470 AA.
AC 061382;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Cysteine rich motif associated to Ring and Traf domains protein
DE (MCAFI1).
GN TRAF4 OR CARL1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-98175886; PubMed-9507120;
RA Masson R., Regnier C.H., Chenard M.P., Wendling C., Mattei M.G.,
RA Tomasello C., Rio M.C.;
RT "Tumor necrosis factor receptor associated factor4 (TRAF4) expression
RT pattern during mouse development.";
RL Mech. Dev. 71:187-191(1998).
CC -1 SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: X92346; CAA63103.1;
DR MGD: MGI:1202880; Tiaf4.
DR InterPro: IPR002083; MATH.
DR InterPro: IPR003007; TRAF.
DR InterPro: IPR001841; znf_ring.
DR InterPro: IPR001293; znf_TRAF.
DR Pfam: PF00917; MATH; 1.
DR Pfam: PF00097; zf-C3HC4; 1.
DR Pfam: PF02176; zf-TRAF; 3.
DR SMART: SM00061; MATH; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS00518; zf_RING_1; 1.
KW Zinc-finger.
SQ
SEQUENCE 470 AA: 53418 MW: 842P2168A926BAFB CRC64;

Query Match 17.4%; Score 524.5; DB 11; Length 470;
Best Local Similarity 24.1%; Pred. No. 3, 4e-25;
Matches 142; Conservative 75; Mismatches 178; Indels 195; Gaps 13;

OY 38 GYKEKYKVEDEKYEKCHLVLCSPKQTEGCHRFCECMAALLSSSPKCTACQESIV 96
DB 3 GLDYKPRPEKRYRLCLPRLCGKPRMDSVEVSTCGHRYCDNCLQELFSEGVFKCPEDQLPD 62
OY 97 KDVFKNCKCKRELLAOIYCRNBSRGAQOLILGLHLVILKNDKCFEELPCVRP--CKE 155
DB 63 YAKIYRPELEVOYLALICITISEECGRNSGRLHDOGLH--NTGSFNVVPC--PVRCPA 119
OY 156 KVLKLDRLHVEKAKYREATCSHCKSOVMIALQKH----- 193
DB 120 KLSRRDLRALHNDCKRRLKCEFGCDPSGEAVESHGVCQESVFCENKCGAKMRRL 179
OY 194 -----DT-----DCCVVVSCPHKCSVOTLLRSELNHL 222
DB 180 LAOHATSECKRPQPCAYCTKEFVYDTIOSHOYQCPRLVPCPNQCGVTVAREDPRTL 239
OY 223 SE--CVNAPSTCSFKRGCVFOGTNOQIKAHESASAVOHVNLKEMSNSLEKKVSLQNS 281
DB 240 KDCSRFAFYLCPRKESGCKHRCKLAKGRHVESVAPHLAM----- 281
OY 282 VEKNKSIQSLHNOICFELIEEROKEMLRNNSKILHLQVIDSOAKELKELDKELRPR 341
DB 282 -----CA-----LVSRQQLDELRLREL----- 299
OY 342 QNMEEADSKSSVESIQNRVTELSVDKSAQOVARNTGLLESOLSRHDOMLSVHDIRLAD 401

```

```

Db 300 -----EELSI----- 304
Qy 402 MDLRFVLETSYNGVLIWKIRDKRRKOEAVMGKTLISYQPPYTGFGKRCARVYLN 461
Db 305 -----GSDGVLIWKIGSYGRRLQEKAKPNLECFSPAFYTHYGYKLVASLN 353
Qy 462 GDGMKRGTHLSFFVIMGEVDALLPMPFKOKVITLMDG-----SSRHLGDAFKDPNP 517
Db 354 GNGSEGHLSIYIRVLFGLAFDNLLEWPLARVYFSLDQSDPLAKQFHVTEFHPDPN 413
Qy 518 SSFFKKP-----TGMNIASGCPVFAQVYLENGYIKDITFIKVIYD 561
Db 414 WKNFQKPGTWGSGIDESSLGFGYKPKFISHODIRKKNRYRDAVFLASVE 463

RESULT 12
Q9BIW7 PRELIMINARY; PRT; 462 AA.
ID 09BIW7
AC 09BIW7
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE TRF-1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21407711; PubMed=11516642;
RA Pulol N., Link E.M., Liu L.X., Kurz C.L., Allong G., Tan M.,
RA Ray K.P., Solari R., Johnson C.D., Ewbank J.J.;
RT "A reverse genetic analysis of components of the Toll signaling
RT pathway in Caenorhabditis elegans.";
RL Curr. Biol. 11:809-821(2001).
DR EMBL: AF348168; AAK37546.1; -.
DR InterPro: IPR002083; MATH.
DR InterPro: IPR003007; TRAF.
DR InterPro: IPR001841; ZnF_ZnF.
DR InterPro: IPR001293; ZnF_TRAF.
DR Pfam: PF00917; MATH; 1.
DR Pfam: PF02176; zf-TRAF; 2.
DR SMART: SM00061; MATH; 1.
DR SMART: SM00184; RING; 1.
SQ SEQUENCE 462 AA; 52354 MW; E07F04BF1756B343 CRC64;

Query Match 17.4%; Score 522.5; DB 5; Length 462;
Best Local Similarity 26.1%; Pred. No. 4.5e-25;
Matches 136; Conservative 69; Mismatches 188; Indels 129; Gaps 12;

Qy 53 CECHLVLSCKQTEGHRFCESMAALLSSSPKCTACQESIVDKVFNCKCKRELLA 112
Db 18 CPICEQALRDPIKLNCDHNYRCQCFEN--ENRTGCAACOTTIOPELCOHDKAKOKOILA 75
Qy 113 LOIYCRNESCRCAGDLTGLHLVHLKNDCHFE-ELPCVRPDCKEVLRKDLRDHYEKAC 171
Db 76 LPVVCFFESSGCPWMDQGLTLDHL-SECTFKSSLKCK--CGRQFAKNLDEKHKRAK-CE 131
Qy 172 YREATCSHCKSQVPMALOKHEDTDCPVVSCPHKCSVOTLRLSELSAHLSECVNAPST 231
Db 132 LNRVAVCSFCNKTIIRDSDRHRPKT-CPQVITISCFQGLDRLPRLEIEAHCSCPVNDV 190
Qy 232 CSKRRGCVFGOTNOQIKAHSSAIVHNLKEMSNLEKVSLLQNSVEKNKSISQSL 291
Db 191 CPEVPYGTCTFAGKESIQHLSDEVRHLMYLCDEITDLKGYELM----- 236
Qy 292 HNQISFEIEIRQKEMLRNNEKILHQRVIDSOAEKIKELDKETIRPFRQNWSEADSMK 351
Db 237 -----ERDMGSPNDROTIRL-----SAAETCTEM----- 260
Qy 352 SSVESLQNRVTELESVDKSGAGVARTGLLESQLSRHDOMLSVHDIRLADMILRQVLET 411
Db 261 ----- 260

```

```

Qy 412 ASYNGVLIWKIRDKRRKOEAVMGKTLISYQPPYTGFGKRCARVYLNDGMKGTHL 471
Db 261 --REPOLIKWIDKLOQRTNNAKSGADTTIFSVFPHHRRGYKMMACALFGSSSAGKSI 318
Qy 472 STEFVIMGEVDALLPMPFKOKVITLMDG-----SSRHLGDAFKDPNPSSSKKPT 525
Db 319 SLVYLLKGEFDPTLEWPFHRAIKISLDONPRPEDRVNITVYIDPRKLKANKFLARPR 378
Qy 526 GEMNIASGCPVFAQVYLENGYIKDITFIKVIYDTSO-LP 566
Db 379 GERNAAGSOSFESLALLO--YKDKDIYQIDVDKCEITLP 418

RESULT 13
ID 062248 PRELIMINARY; PRT; 509 AA.
AC 062248
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE F45G2.6 protein.
GN F45G2.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RX Lindsey S.J.;
RL submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C. elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL: Z93382; CAB07615.1; -.
DR InterPro: IPR002083; MATH.
DR InterPro: IPR003007; TRAF.
DR InterPro: IPR001841; ZnF_ZnF.
DR InterPro: IPR001293; ZnF_TRAF.
DR Pfam: PF00917; MATH; 1.
DR Pfam: PF02176; zf-TRAF; 2.
DR SMART: SM00061; MATH; 1.
DR SMART: SM00184; RING; 1.
SQ SEQUENCE 509 AA; 57514 MW; CFA0E068F5AD00C8 CRC64;

Query Match 17.4%; Score 522.5; DB 5; Length 509;
Best Local Similarity 26.1%; Pred. No. 5e-25;
Matches 136; Conservative 69; Mismatches 188; Indels 129; Gaps 12;

Qy 53 CECHLVLSCKQTEGHRFCESMAALLSSSPKCTACQESIVDKVFNCKCKRELLA 112
Db 65 CPICEQALRDPIKLNCDHNYRCQCFEN--ENRTGCAACOTTIOPELCOHDKAKOKOILA 122
Qy 113 LOIYCRNESCRCAGDLTGLHLVHLKNDCHFE-ELPCVRPDCKEVLRKDLRDHYEKAC 171
Db 123 LPVVCFFESSGCPWMDQGLTLDHL-SECTFKSSLKCK--CGRQFAKNLDEKHKRAK-CE 178
Qy 172 YREATCSHCKSQVPMALOKHEDTDCPVVSCPHKCSVOTLRLSELSAHLSECVNAPST 231
Db 179 LNRVAVCSFCNKTIIRDSDRHRPKT-CPQVITISCFQGLDRLPRLEIEAHCSCPVNDV 237
Qy 232 CSKRRGCVFGOTNOQIKAHSSAIVHNLKEMSNLEKVSLLQNSVEKNKSISQSL 291
Db 238 CPEVPYGTCTFAGKESIQHLSDEVRHLMYLCDEITDLKGYELM----- 283
Qy 292 HNQISFEIEIRQKEMLRNNEKILHQRVIDSOAEKIKELDKETIRPFRQNWSEADSMK 351
Db 284 -----ERDMGSPNDROTIRL-----SAAETCTEM----- 307

```



```

QY 352 SVSEIQNNVTELESVDKSGAGVARNITGLLESQLSRHDQMLSVHDIRLADMDLRFVLETA 411
Db 308 ----- 307
QY 412 ASYNGVLINKIRDKRRKROAVNGKTLISYQPFYTGYYKMCARVYNGDGKGTJLH 471
Db 308 --FEPOLIMIKIDKIQOQTNEAKSGADTTTFYFPMHSRGGYKMMACACILFGDGSAGKSI 365
QY 472 SLFEVINGEYDALLPMPFKOKVTLMMDQGS-----SRRLHGAFFKDPSSSEFKPT 525
Db 366 SLVYLLKGFDPTELEPFIRAKISLLQONPREPDRVITTYVIDPRKLAKNEKFLARPR 425
QY 526 GEMNINSGCFVFAQTVLENGYTIKDTIFIKVYDTS-DLP 566
Db 426 GERNAFSGSFCSLAIQNN--YKDKDKIVQIDVDRCETLP 465

RESULT 14
QYXR0 PRELIMINARY: PRT: 486 AA.
AC QYXR0:
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE TRAF1 protein (L20987P).
GN TRAF1 OR CG3048.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxId=7227;
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Barker E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abrell J.F., Agbayani A., An H.-J., Andrews-Pfannoch C., Baldwin D.,
RA Baller R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borczyk D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Butts K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Gelbart W.M., Glaesner W.,
RA Foster C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glaesner W.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris K.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Jaislin M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lazo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Maitel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner C., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).

```

---

```

RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99147085; PubMed=10021364;
RA Liu H., Su Y.C., Becker E., Treisman J., Skolnik E.Y.;
RT "A Drosophila TNF-receptor-associated factor (TRAF) binds the src20
RT kinase Mischaplan and activates Jun kinase."
RL Curr. Biol. 9:101-104(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farrant D., Fritze E.,
RA George R., Gonzalez M., Guanin H., Krommiller B., Li P., Lao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celinker S.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AEO03576; AAF51024.1; -
DR EMBL: AF119794; AAD34346.1; -
DR EMBL: AY094792; AAM1145.1; -
DR Flybase: FBgn0026319; TrAF1.
DR InterPro: IPR002083; MATH.
DR InterPro: IPR003007; TRAF.
DR InterPro: IPR001293; ZnF-TRAF.
DR Pfam: PR00917; MATH; 1.
DR Pfam: PR02176; ZF-TRAF; 3.
DR SMART: SM00061; MATH; 1.
DR Receptor.
KW SEQUENCE 486 AA; 53665 MW; 41474B5E014A9D5 CRC64;

Query Match 16.8%; Score 506; DB 5; Length 486;
Best Local Similarity 24.3%; Pred. No. 5.2e-24;
Matches 140; Conservative 77; Mismatches 187; Indels 172; Gaps 13;
QY 3 SSKKNDSPGALQTNPL-KLHTDSAGTPVPEEGGKYEKFTVDDKYCE----- 54
Db 67 SSSPTPCNNNNNNPIELBQIIPG-----PDKHMSLVLCIHHKGGCKMSDLRK 121
QY 55 -KCHLVSPKPTGEGHFCSCMAALLSSSPKCTAQESIVKDYKFNCCRETLAL 113
Db 122 LGHNLNACKHDATQCPN-----KCGAIDPRIMTDLQYCTCTMRRTRC- 164
QY 114 QYICRNESGCAEQTLTGLHLVHLKNDCHFEELPCVPRDCKEYLRKDLNDHYEKAKYR 173
Db 165 -EFCQSEFSGAG-----LEHNGSGGQPEVTC-EAKGQRLRKRMTLHNSKDCAKR 214
QY 174 EATCSCHCKSQVPMALQKHEDTDCPVVNSCPHKSQVOTLRSELNAHL-SECVNAPSTC 232
Db 215 LIRCAHCOREFSADTLPPLHA-AQCPRAPLACQPCDAGPIPRGELNHLNDECOISLAVSC 273
QY 223 SFKRGVCFOGTNOQIKRHESSAVQVNLKENSLEKRVSLQNESVEKNKKSIOSLH 292
Db 274 SFKEGCGCFKPRQMLEHLSNAHLSLVVALSSRQGOIOIML----- 318
QY 293 NOICFEIEIEROKEMLRNNSKILHLQVYDSQAELKELDEIRFRQNMEEADSMKS 352
Db 319 ----- 320
QY 320 SVSEIQNNVTELESVDKSGAGVARNITGLLESQLSRHDQMLSVHDIRLADMDLRFVLETA 412
Db 321 AVSKL-----SI 327
QY 413 SYNGVLINKIRDKRRKROAVNGKTLISYQPFYTGYYKMCARVYNGDGKGTJLH 472
Db 328 NYTGILLKIKIDMSAKAERKAGDGLVSPPTTYQYGIKLOASMFLLNGNGEWTWHS 387
QY 473 LFEVINGEYDALLPMPFKOKVTLMMDQGS-----SRRLHGAFFKDPSSSEFKPTGEN- 529
Db 388 VYIKVLGCEYDALLKMPFSHTSTFTFLEQGAQSGQGVASFPDPDTWENFQPSNEPQ 447
QY 530 IASCPVFAQTVLENGYTIKDTIFIKVYDTS-DLP 565
Db 448 LGFEPFRISHELHSPRIKIDTVFLRVKVPDSKI 483

```

RESULT 15

ID Q9UAC5 PRELIMINARY; PRT: 412 AA.

AC Q9UAC5; 01-MAY-2000 (Tremblrel. 13, Created)

DT 01-MAY-2000 (Tremblrel. 13, last sequence update)

DT 01-MAR-2002 (Tremblrel. 20, last annotation update)

DE TRAF1.

GN TRAF1 OR CG3048.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

CX NCBI\_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RA Medzhitov R., Janeway C.;

RT "Drosophila TRAF proteins are components of innate host defense

paths."

RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF079837; AAD47894.1; -

DR EMBL: AF111422; AAG21891.1; -

DR FlyBase; FBgn0026319; Traf1.

DR InterPro; IPR002083; MATH.

DR InterPro; IPR003007; TRAF.

DR Pfam; PF00917; MATH; 1.

DR Pfam; PF02176; zf-TRAF; 3.

DR SMART; SMO0061; MATH; 1.

SQ SEQUENCE 412 AA; 46159 MW; 81A05147AA7D64CE CRC64;

Query Match 16.7%; Score 503; DB 5; Length 412;

Best Local Similarity 24.8%; Pred. No. 6; Se-24;

Matches 129; Conservative 73; Mismatches 161; Indels 158; Gaps 10;

QY 49 DKYKCKHLYVCSKPCFCEGSCMAALLSSSPKCTACQESIYKDKVFKNCKR 108  
 DB 43 DELKRLKGLHNAKCKHDATQCPN-----KCGAQIPRIMMDHLDQYCTMR 86  
 QY 109 EILALQIYCRNESRGCAQLTGLHLVHLKNDCHPEELPCVPRDCKEVLKRLDHYEK 168  
 DB 87 RTRC--EFCQSEFSGAG-----LEEHNGSCGQEPYTC-EAKCGQRILGRMTLHRSK 135  
 QY 169 ACKYRATCSHKCSQVPMIALOKHEDTDCPCVVSCHPKCSVOTLLRSELSAHL-SECVN 227  
 DB 136 DCAKRLRCACHQRESADTLPILHA-AQCPRAPLACPCRCAGPIPRGELAHLRDECQS 194  
 QY 228 APTCSFKRYGCVFQGTNOQIKAHBASAVOHVNLKEMNSLEKVSLLONESVEKNKS 287  
 DB 195 LAVSCSFKAGRGFKGPRQMLFAHLESNAAHLSIMVALSSROGOIOML----- 244  
 QY 288 IGSLNQICSPLEIFRQKEMLRNNESEKILHQRVIDSQAEKLEKELDEIRPFQNWEEA 347  
 DB 245 ----- 244  
 QY 348 DSMKSSVESLONRVTELESVDKSGAVARNTGLLESQLSRHDOMLSVHDIRLADMDFQ 407  
 DB 245 ---KSAVSKL----- 251  
 QY 408 VLEFASVNGVLLWKIRDYRRKQEAVMGKTLISOPFTTGFGYKMCARYVINDGCMGK 467  
 DB 252 ---SINTGTLLWKITDWSAKMAEAGKDELIVSPFTSQYGYKIQASMFNLNGNGPGE 308  
 QY 468 GTHLISLFEVIMRGEVDALLPMPEKQKVTLMLDQG--SSRHLGDAFKPDPSSSFKKPT 525  
 DB 309 NTHVSYIKVLPGEYDALIKWPSHSITTLFEQCAQSGGQVAFSPDPPTWENFORPS 368

QY 526 GEMN-IASGCPVPAQTVLENGYIKDDTIFIKYIVDFSDL 565  
 DB 369 NEPDQLGFGFPFRFISHLHSPPIKIGDTVFLRKAVDPSKI 409

Search completed: December 19, 2002, 14:55:32  
 Job time : 42 secs